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RAW SEQUENCE LISTING

DATE: 10/09/2001

PATENT APPLICATION: US/09/954,679

TIME: 06:11:22

Input Set : A:\ES.txt

Output Set: N:\CRF3\10092001\I954679.raw

3 <110> APPLICANT: Donna T. Ward
4 Andrew T. Watt
6 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF RIBONUCLEASE L (2',5'-
OLIGOISODENYLATE

7 SYNTHETASE-DEPENDENT) EXPRESSION
9 <130> FILE REFERENCE: RTS-0212
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/954,679
C--> 11 <141> CURRENT FILING DATE: 2001-09-12

ENTERED

11 <160> NUMBER OF SEQ ID NOS: 88

14 <210> SEQ ID NO: 1

15 <211> LENGTH: 20

16 <212> TYPE: DNA

17 <213> ORGANISM: Artificial Sequence

19 <220> FEATURE:

21 <223> OTHER INFORMATION: Antisense Oligonucleotide ✓

23 <400> SEQUENCE: 1

24 tccgtcatcg ctctcaggg

20

27 <210> SEQ ID NO: 2

28 <211> LENGTH: 20

29 <212> TYPE: DNA

30 <213> ORGANISM: Artificial Sequence ✓

32 <220> FEATURE:

34 <223> OTHER INFORMATION: Antisense Oligonucleotide ✓

36 <400> SEQUENCE: 2

37 atgcattctg cccccaagga

20

40 <210> SEQ ID NO: 3

41 <211> LENGTH: 2928

42 <212> TYPE: DNA

43 <213> ORGANISM: Homo sapiens

45 <220> FEATURE:

47 <220> FEATURE:

48 <221> NAME/KEY: CDS

49 <222> LOCATION: (104)...(2329)

51 <400> SEQUENCE: 3

52 aatcccaact tacactcaaaa gcttctttga ttaagtgcta ggagataaat ttgcattttc 60

54 tcaaggaaaa ggctaaaagt ggtagcaggt ggcatttacc gtc atg gag agc agg 115

Met Glu Ser Arg

55 1

58 gat cat aac aac ccc cag gag gga ccc acg tcc tcc agc ggt aga agg 163

59 Asp His Asn Asn Pro Gln Glu Gly Pro Thr Ser Ser Ser Gly Arg Arg

60 5 10 15 20

62 gct gca gtg gaa gac aat cac ttg ctg att aaa gct gtt caa aac gaa 211

63 Ala Ala Val Glu Asp Asn His Leu Leu Ile Lys Ala Val Gln Asn Glu

64 25 30 35

66 gat gtt gac ctg gtc cag caa ttg ctg gaa ggt gga gcc aat gtt aat 259

67 Asp Val Asp Leu Val Gln Gln Leu Leu Glu Gly Gly Ala Asn Val Asn

68 40 45 50

70 ttc cag gaa gag gaa ggg ggc tgg aca cct ctg cat aac gca gta caa 307

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71 Phe Gln Glu Glu Gly Gly Trp Thr Pro Leu His Asn Ala Val Gln
72          55          60          65
74 atg agc agg gag gac att gtg gaa ctt ctg ctt cgt cat ggt gct gac      355
75 Met Ser Arg Glu Asp Ile Val Glu Leu Leu Leu Arg His Gly Ala Asp
76          70          75          80
78 cct gtt ctg agg aag aag aat ggg gcc acg cct ttt atc ctc gca gcg      403
79 Pro Val Leu Arg Lys Lys Asn Gly Ala Thr Pro Phe Ile Leu Ala Ala
80 85          90          95          100
82 att gcg ggg agc gtg aag ctg ctg aaa ctt ttc ctt tct aaa gga gca      451
83 Ile Ala Gly Ser Val Lys Leu Leu Lys Leu Phe Leu Ser Lys Gly Ala
84          105          110          115
86 gat gtc aat gag tgt gat ttt tat ggc ttc aca gcc ttc atg gaa gcc      499
87 Asp Val Asn Glu Cys Asp Phe Tyr Gly Phe Thr Ala Phe Met Glu Ala
88          120          125          130
90 gct gtg tat ggt aag gtc aaa gcc cta aaa ttc ctt tat aag aga gga      547
91 Ala Val Tyr Gly Lys Val Lys Ala Leu Lys Phe Leu Tyr Lys Arg Gly
92          135          140          145
94 gca aat gtg aat ttg agg cga aag aca aag gag gat caa gag cgg ctg      595
95 Ala Asn Val Asn Leu Arg Arg Lys Thr Lys Glu Asp Gln Glu Arg Leu
96          150          155          160
98 agg aaa gga ggg gcc aca gct ctc atg gac gct gct gaa aaa gga cac      643
99 Arg Lys Gly Gly Ala Thr Ala Leu Met Asp Ala Ala Glu Lys Gly His
100 165          170          175          180
102 gta gag gtc ttg aag att ctc ctt gat gag atg ggg gca gat gta aac      691
103 Val Glu Val Leu Lys Ile Leu Leu Asp Glu Met Gly Ala Asp Val Asn
104          185          190          195
106 gcc tgt gac aat atg ggc aga aat gcc ttg atc cat gct ctc ctg agc      739
107 Ala Cys Asp Asn Met Gly Arg Asn Ala Leu Ile His Ala Leu Leu Ser
108          200          205          210
110 tct gac gat agt gat gtg gag gct att acg cat ctg ctg ctg gac cat      787
111 Ser Asp Asp Ser Asp Val Glu Ala Ile Thr His Leu Leu Leu Asp His
112          215          220          225
114 ggg gct gat gtc aat gtg agg gga gaa aga ggg aag act ccc ctg atc      835
115 Gly Ala Asp Val Asn Val Arg Gly Glu Arg Gly Lys Thr Pro Leu Ile
116          230          235          240
118 ctg gca gtg gag aag aag cac ttg ggt ttg gtg cag agg ctt ctg gag      883
119 Leu Ala Val Glu Lys Lys His Leu Gly Leu Val Gln Arg Leu Leu Glu
120 245          250          255          260
122 caa gag cac ata gag att aat gac aca gac agt gat ggc aaa aca gca      931
123 Gln Glu His Ile Glu Ile Asn Asp Thr Asp Ser Asp Gly Lys Thr Ala
124          265          270          275
126 ctg ctg ctt gct gtt gaa ctc aaa ctg aag aaa atc gcc gag ttg ctg      979
127 Leu Leu Leu Ala Val Glu Leu Lys Leu Lys Lys Ile Ala Glu Leu Leu
128          280          285          290
130 tgc aaa cgt gga gcc agt aca gat tgt ggg gat ctt gtt atg aca gcg      1027
131 Cys Lys Arg Gly Ala Ser Thr Asp Cys Gly Asp Leu Val Met Thr Ala
132          295          300          305
134 agg cgg aat tat gac cat tcc ctt gtg aag gtt ctt ctc tct cat gga      1075
135 Arg Arg Asn Tyr Asp His Ser Leu Val Lys Val Leu Leu Ser His Gly

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136	310	315	320	
138	gcc aaa gaa gat ttt cac cct cct gct gaa gac tgg aag cct cag agc	1123		
139	Ala Lys Glu Asp Phe His Pro Pro Ala Glu Asp Trp Lys Pro Gln Ser			
140	325 330 335 340			
142	tca cac tgg ggg gca gcc ctg aag gat ctc cac aga ata tac cgc cct	1171		
143	Ser His Trp Gly Ala Ala Leu Lys Asp Leu His Arg Ile Tyr Arg Pro			
144	345 350 355			
146	atg att ggc aaa ctc aag ttc ttt att gat gaa aaa tac aaa att gct	1219		
147	Met Ile Gly Lys Leu Lys Phe Phe Ile Asp Glu Lys Tyr Lys Ile Ala			
148	360 365 370			
150	gat act tca gaa gga ggc atc tac ctg ggg ttc tat gag aag caa gaa	1267		
151	Asp Thr Ser Glu Gly Gly Ile Tyr Leu Gly Phe Tyr Glu Lys Gln Glu			
152	375 380 385			
154	gta gct gtg aag acg ttc tgt gag ggc agc cca cgt gca cag cgg gaa	1315		
155	Val Ala Val Lys Thr Phe Cys Glu Gly Ser Pro Arg Ala Gln Arg Glu			
156	390 395 400			
158	gtc tct tgt ctg caa agc agc cga gag aac agt cac ttg gtg aca ttc	1363		
159	Val Ser Cys Leu Gln Ser Ser Arg Glu Asn Ser His Leu Val Thr Phe			
160	405 410 415 420			
162	tat ggg agt gag agc cac agg ggc cac ttg ttt gtg tgt gtc acc ctc	1411		
163	Tyr Gly Ser Glu Ser His Arg Gly His Leu Phe Val Cys Val Thr Leu			
164	425 430 435			
166	tgt gag cag act ctg gaa gcg tgt ttg gat gtg cac aga ggg gaa gat	1459		
167	Cys Glu Gln Thr Leu Glu Ala Cys Leu Asp Val His Arg Gly Glu Asp			
168	440 445 450			
170	gtg gaa aat gag gaa gat gaa ttt gcc cga aat gtc ctg tca tct ata	1507		
171	Val Glu Asn Glu Glu Asp Glu Phe Ala Arg Asn Val Leu Ser Ser Ile			
172	455 460 465			
174	ttt aag gct gtt caa gaa cta cac ttg tcc tgt gga tac acc cac cag	1555		
175	Phe Lys Ala Val Gln Glu Leu His Leu Ser Cys Gly Tyr Thr His Gln			
176	470 475 480			
178	gat ctg caa cca caa aac atc tta ata gat tct aag aaa gct gct cac	1603		
179	Asp Leu Gln Pro Gln Asn Ile Leu Ile Asp Ser Lys Lys Ala Ala His			
180	485 490 495 500			
182	ctg gca gat ttt gat aag agc atc aag tgg gct gga gat cca cag gaa	1651		
183	Leu Ala Asp Phe Asp Lys Ser Ile Lys Trp Ala Gly Asp Pro Gln Glu			
184	505 510 515			
186	gtc aag aga gat cta gag gac ctt gga cgg ctg gtc ctc tat gtg gta	1699		
187	Val Lys Arg Asp Leu Glu Asp Leu Gly Arg Leu Val Leu Tyr Val Val			
188	520 525 530			
190	aag aag gga agc atc tca ttt gag gat ctg aaa gct caa agt aat gaa	1747		
191	Lys Lys Gly Ser Ile Ser Phe Glu Asp Leu Lys Ala Gln Ser Asn Glu			
192	535 540 545			
194	gag gtg gtt caa ctt tct cca gat gag gaa act aag gac ctc att cat	1795		
195	Glu Val Val Gln Leu Ser Pro Asp Glu Glu Thr Lys Asp Leu Ile His			
196	550 555 560			
198	cgt ctc ttc cat cct ggg gaa cat gtg agg gac tgt ctg agt gac ctg	1843		
199	Arg Leu Phe His Pro Gly Glu His Val Arg Asp Cys Leu Ser Asp Leu			
200	565 570 575 580			

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202 ctg ggt cat ccc ttc ttt tgg act tgg gag agc cgc tat agg acg ctt      1891
203 Leu Gly His Pro Phe Phe Trp Thr Trp Glu Ser Arg Tyr Arg Thr Leu
204                               585                               590                               595
206 cgg aat gtg gga aat gaa tcc gac atc aaa aca cga aaa tct gaa agt      1939
207 Arg Asn Val Gly Asn Glu Ser Asp Ile Lys Thr Arg Lys Ser Glu Ser
208                               600                               605                               610
210 gag atc ctc aga cta ctg caa cct ggg cct tct gaa cat tcc aaa agt      1987
211 Glu Ile Leu Arg Leu Leu Gln Pro Gly Pro Ser Glu His Ser Lys Ser
212                               615                               620                               625
214 ttt gac aag tgg acg act aag att aat gaa tgt gtt atg aaa aaa atg      2035
215 Phe Asp Lys Trp Thr Thr Lys Ile Asn Glu Cys Val Met Lys Lys Met
216                               630                               635                               640
218 aat aag ttt tat gaa aaa aga ggc aat ttc tac cag aac act gtg ggt      2083
219 Asn Lys Phe Tyr Glu Lys Arg Gly Asn Phe Tyr Gln Asn Thr Val Gly
220 645                               650                               655                               660
222 gat ctg cta aag ttc atc cgg aat ttg gga gaa cac att gat gaa gaa      2131
223 Asp Leu Leu Lys Phe Ile Arg Asn Leu Gly Glu His Ile Asp Glu Glu
224                               665                               670                               675
226 aag cat aaa aag atg aaa tta aaa att gga gac cct tcc ctg tat ttt      2179
227 Lys His Lys Lys Met Lys Leu Lys Ile Gly Asp Pro Ser Leu Tyr Phe
228                               680                               685                               690
230 cag aag aca ttt cca gat ctg gtg atc tat gtc tac aca aaa cta cag      2227
231 Gln Lys Thr Phe Pro Asp Leu Val Ile Tyr Val Tyr Thr Lys Leu Gln
232                               695                               700                               705
234 aac aca gaa tat aga aag cat ttc ccc caa acc cac agt cca aac aaa      2275
235 Asn Thr Glu Tyr Arg Lys His Phe Pro Gln Thr His Ser Pro Asn Lys
236                               710                               715                               720
238 cct cag tgt gat gga gct ggt ggg gcc agt ggg ttg gcc agc cct ggg      2323
239 Pro Gln Cys Asp Gly Ala Gly Gly Ala Ser Gly Leu Ala Ser Pro Gly
240 725                               730                               735                               740
242 tgc tga tggactgatt tgctggagtt caggggaacta cttattagct gtagagtcct      2379
243 Cys
246 tggcaaatca caacattctg ggccttttaa ctcaccagggt tgcttgtagg ggaatgagttg      2439
248 catagctgat atgtcagttc ctggcatcgt gtattccata tgtctataac aaaagcaata      2499
250 tatacccaga ctacactagt ccataagcct taccactaa ctgggaggac attctgctaa      2559
252 gattcctttt gtcaattgca ccaaaagaat gagtgccttg acccctaatt ctgcatatgt      2619
254 tacaattctc tcaatttaatt ttcccaatga tcttgcaaaa cagggattat catccccatt      2679
256 taagaactga ggaacctgag actcagagag tgtgagctac tggcccaaga ttattcaatt      2739
258 tatacctagc actttataaa tttatgtggt gttattggta cctctcattt gggcacctta      2799
260 aaacttaact atcttccagg gctcttcag atgaggccca aaacatatat aggggttcca      2859
262 ggaatctcat tcattcattc agtattttatt gagcatctag tataagtctg ggcactggat      2919
264 gcatgaatt                                                                2928
267 <210> SEQ ID NO: 4
268 <211> LENGTH: 21
269 <212> TYPE: DNA
270 <213> ORGANISM: Artificial Sequence
272 <220> FEATURE:
274 <223> OTHER INFORMATION: PCR Primer
276 <400> SEQUENCE: 4

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277 ctgagtgacc tgctgggtca t 21
280 <210> SEQ ID NO: 5
281 <211> LENGTH: 21
282 <212> TYPE: DNA
283 <213> ORGANISM: Artificial Sequence
285 <220> FEATURE:
287 <223> OTHER INFORMATION: PCR Primer
289 <400> SEQUENCE: 5
290 tcggattcat ttcccacatt c 21
293 <210> SEQ ID NO: 6
294 <211> LENGTH: 28
295 <212> TYPE: DNA
296 <213> ORGANISM: Artificial Sequence
298 <220> FEATURE:
300 <223> OTHER INFORMATION: PCR Probe
302 <400> SEQUENCE: 6
303 tcctatagcg gctctcccaa gtccaaaa 28
306 <210> SEQ ID NO: 7
307 <211> LENGTH: 19
308 <212> TYPE: DNA
309 <213> ORGANISM: Artificial Sequence
311 <220> FEATURE:
313 <223> OTHER INFORMATION: PCR Primer
315 <400> SEQUENCE: 7
316 gaaggtgaag gtcggagtc 19
319 <210> SEQ ID NO: 8
320 <211> LENGTH: 20
321 <212> TYPE: DNA
322 <213> ORGANISM: Artificial Sequence
324 <220> FEATURE:
326 <223> OTHER INFORMATION: PCR Primer
328 <400> SEQUENCE: 8
329 gaagatggtg atgggatttc 20
332 <210> SEQ ID NO: 9
333 <211> LENGTH: 20
334 <212> TYPE: DNA
335 <213> ORGANISM: Artificial Sequence
337 <220> FEATURE:
339 <223> OTHER INFORMATION: PCR Probe
341 <400> SEQUENCE: 9
342 caagcttccc gttctcagcc 20
345 <210> SEQ ID NO: 10
346 <211> LENGTH: 447
347 <212> TYPE: DNA
348 <213> ORGANISM: Homo sapiens
350 <220> FEATURE:
353 <400> SEQUENCE: 10
354 cacgagggaa actgctcggg atgcaagcag tcttccaggc tttgcggttg ccacaggaat 60
356 aattgatacg tctgagttga gcagggtggaa tgtcaaaaaa ctgaaaacat tgttccttct 120

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VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date